

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 28, 2002, 08:01:00 ; Search time 2751.06 Seconds
(without alignments)
12197.381 Million cell updates/sec

Title: US-08-711-417C-165

Perfect score: 1551

Sequence: 1 ATGAGCTCTGACGAGGTCA.....ACGGTTCACATGAGCTAA 1551

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 21979536 seqs, 10817449327 residues

Total number of hits satisfying chosen parameters: 43959072

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending_Patents_NA_Main:*

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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1551	100.0	1788	18	US-09-435-327A-19	Sequence 19, Appl
2	1497.8	96.6	6171	56	US-60-172-373-18124	Sequence 18124, A
3	1468.8	94.7	3629	14	US-09-023-655-923	Sequence 923, App
4	1468.8	94.7	3629	18	US-09-435-327A-18	Sequence 18, Appl
5	1468.8	94.7	3629	18	US-09-442-384A-721	Sequence 721, Appl
6	1468.8	94.7	4786	25	US-09-649-161-10365	Sequence 10365, A
7	1468.8	94.7	4786	25	US-09-652-816-9158	Sequence 9158, Ap
8	1468.8	94.7	4786	27	US-09-698-013-6274	Sequence 6274, Ap
9	1468.8	94.7	4786	27	US-09-698-014-4890	Sequence 4890, Ap
10	1468.8	94.7	4786	28	US-09-717-350-5922	Sequence 5922, Ap
11	1468.8	94.7	4786	29	US-09-726-802-2123	Sequence 2123, Ap
12	1468.8	94.7	4786	29	US-09-726-811-4096	Sequence 4096, Ap
13	1457.8	94.0	6203	71	US-60-324-185-24401	Sequence 24401, A
14	1386	89.4	1386	1	PCT-US99-02559-16	Sequence 16, Appl
15	1386	89.4	1386	6	US-08-238-212A-3	Sequence 3, Appl
16	1386	89.4	1386	8	US-08-465-590B-3	Sequence 3, Appl
17	1386	89.4	1386	11	US-08-733-622A-16	Sequence 16, Appl
18	1386	89.4	1386	11	US-08-733-622B-16	Sequence 16, Appl
19	1386	89.4	1386	14	US-09-019-348-16	Sequence 16, Appl
20	1386	89.4	1386	14	US-09-019-348A-16	Sequence 16, Appl
21	1386	89.4	1386	29	US-09-755-830-2	Sequence 2, Appl
22	1382.4	89.1	1611	5	US-08-121-438-3	Sequence 3, Appl
23	1174.8	75.7	2049	1	PCT-US99-02559-18	Sequence 18, Appl
24	1174.8	75.7	2049	6	US-08-238-212A-5	Sequence 5, Appl
25	1174.8	75.7	2049	8	US-08-465-590B-5	Sequence 5, Appl
26	1174.8	75.7	2049	11	US-08-733-622A-18	Sequence 18, Appl
27	1174.8	75.7	2049	11	US-08-733-622B-18	Sequence 18, Appl
28	1174.8	75.7	2049	14	US-09-019-348-18	Sequence 18, Appl
29	1174.8	75.7	2049	14	US-09-019-348A-18	Sequence 18, Appl
30	1174.8	75.7	2049	29	US-09-755-830-4	Sequence 4, Appl
31	868	56.0	1004	1	PCT-US99-02559-21	Sequence 21, Appl

ALIGNMENTS

	Query Match	100.0%	Score 1551;	DB 18;	Length 1788;
	Best Local Similarity	100.0%;	Pred. No. 0;		
	Matches 1551;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	ATGCGTCTGACGAGGGTCAAGACATGCTTTCTCATCAGGGAAGAAAGCCCCCTGTGA	60		
Db	238	atggaatgctgacgaaggttcaagacatgtctttcatcaggaagaaagccccctgtga	297		
QY	61	AGCGATATCTCCAGATGAGGGCGATGAGCCCATGCCGATGCCGATCCCGAGGACGCTCTCCACCA	120		
Db	298	agcgaatctccagatgagggcgatgagccatgpcgatccccgaggacctctccaccacc	357		
QY	121	TCGGGAGGACACGAAGCTTCCAAGAGTCACAGAGTCGTGGCCAGTAAATGTTAAAGTAGAG	180		
Db	358	tcg999ag99acagcaagctccaaagatgacagagtcgtg9ccagtaaatgttaaagtagag	417		
QY	181	ACTCAGAGTGTGAAGAGAAATGGGCGTCCTGTGNAATGATGGGAGAGAAATGTGGCGGAG	240		
Db	418	actcagagtgatgaagagaaatgg99ctg9cctgtgaaatgaaatg999agaaatgtg9c99ag	477		
QY	241	GATTTACGAATGCTTCATGCCCTCGGAGAGAAAATGAATGGCTCCCAAGAGGACCAAGGC	300		
Db	478	gatttcagaaatgcttgatg9cctcg99agagaaaaatgaatgctccacag99gaccaag9c	537		
QY	301	AGCTCGGCTTTGTTCGGGAGTTGGAGCAATTCGACTTCTTACGGAAACATAAAGTGTGAT	360		
Db	538	agctcg9ctt9tc999ag9tt99ag9cattecgacttctcaacg9aaacataa9gt9g9at	597		
QY	361	ATCTGTGGGATCATTTGCATTCGSGGCCAATGTGCTCATGTGTTACAAAAGAGGCACACT	420		
Db	598	atct9t99gatcat9at9catc9999cccaat9t9ctcatg9ttccaaaaaag9ccacact	657		
QY	421	GGAGAACGGCCCCCTCCAGTGTGCAATCAGTGGGGGGCTCATTCACCCAGAAAGGCAACCTG	480		

Db 1738 gagttctgtcgacataacgcgagggagcaccgcttccacatgagctaa 1788

RESULT 2

US-60-172-373-18124
; Sequence 18124, Application US/60172373
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preeti
; APPLICANT: Diep, Dinh
; TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
; FILE REFERENCE: Polynucleotide Sequence Databases, and Single Nucleotide Polymorh
; CURRENT APPLICATION NUMBER: US/60172,373
; CURRENT FILING DATE: 1998-12-16
; NUMBER OF SEQ ID NOS: 25,772
; SOFTWARE: PERL Program
; SEQ ID NO 18124
; LENGTH: 6171
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 345320.3
; NAME/KEY: unsure
; LOCATION: 3401-3583
; OTHER INFORMATION: a, t, c, g, or other
US-60-172-373-18124

Query Match 96.6%; Score 1497.8; DB 56; Length 6171;
Best Local Similarity 98.5%; Pred. No. 1.6e-303;
Matches 1534; Conservative 0; Mismatches 17; Indels 6; Gaps 2;

QY 1 ATGGATGCTCAGCAGGCTCAAGACATGCTCTTCTCATCAGGAGAAAGCCCTCTGTA 60
Db 142 atggaagctgatgaggggtcaagacatgtcccaagtttcaggagaaagagccccctgta 201
QY 61 AGCGATATCTCAGATAGGCGGATGAGCCATGCCGATCCCGAGACCTCTCCACCACC 120
Db 202 agcgatactccagatgagggcgatgagccatgcccagatcccgagacccctccaccacc 261
QY 121 TCGGGAGGACAGCAAGCTCCAGAGTGACAGAGTGCTGGCCAGTAATGTTAAAGTAGAG 180
Db 262 tcg999gagacagaaagctccaaagatgacagagtcgtgcccagtaagttaaagtagag 321
QY 181 ACTCAGATGATCAAGAGAAATGGCGTGCCTGTGAAATGAATGGGAGAAATGTCCGGAG 240
Db 322 actcagatgatgaagagaatggcgctgctggaatgaaatggggaagaatgtgcgag 381
QY 241 GATTTACGAATGCTTGATGCCCTCGGAGAGAAATGAATGGCTCCACAGGACCAAGGC 300
Db 382 gatttacgaatgcttgatgctcgcggagagaaatgaatgctccacagggaccagagc 441
QY 301 AGCTCGGCTTTCTCGGGAGTTGAGGCAATTCGACTTCCTACGGAAACTAAAGTGTGAT 360
Db 442 agctcggttttgcg999gagttgagggcattcgacttccaaacgaaataaagtgtgat 501
QY 361 ATCTGTGGATCATTTGATCGGGCCCAATGTGCTCATGTTTCACAAAGAGCCACACT 420
Db 502 atctgtggaatcattgatcg99cccaatgtgtcaatggttcaaaagaaagcacaact 561
QY 421 GGAGAACGCCCTTCCATGTCGAATCAGTGGGGGCTCATTCACCCAGAGGCAACCTG 480
Db 562 g999aacg99ccctccagtgcattcagtcagtcg99g9ccctcattcccccagagagc 621
QY 481 CTCGGCAGCATCAAGCTCATTCGGGAGAGAGCCCTTCAATGCCACCTCTGCAACTAC 540
Db 622 ctccggacatacaagctgcatcccg99gagagcccttcaaatgccacctctgcaactac 681
QY 541 GCCTGCCCGGAGGAGCGCCCTCACTGGCCACCTGAGGAGCACTCCGTGCTGAACCT 600
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Db 682 gcctgcgcgcg99gagggagcgcctcactg9ccacctgaggacgcactccgttggttaacct 741
QY 601 CACAAATGTGGATATTGTGCCGAAAGCTATAAACAGCAAGCTCTTTAGAGGAACATAAA 660
Db 742 cacaaatgtgtgatatgtg9ccgaagctataaacagcgaacgtcttttagaggaacataaa 801
QY 661 GAGCGCTGCCACAACTACTTGGAAAGCATGGGCTTCCTCCGGGCACACTGTACCCAGTCAT 720
Db 802 g999g9ccacacactcacttggaaagcatg99g9cctccg99gacacactgtaccagtcatt 861
QY 721 AAAGAAGAACTAAGCACAGTGAATGGCAGAGACCTGTGCAAGATAGATGATCAGAGAGA 780
Db 862 aaagaagaactaaagcacagtgaaatggcagaagacctgtgcaagataagatacagagaga 921
QY 781 TCTCTCTGCTGCACAGACTAGCAAGTATATGCGCCAAACGTAAGAGCTCTATGCTCTAG 840
Db 922 tcctctgctgtgacagactagcaagtaagtgcgcaaacgtaagagctctatgctctcag 981
QY 841 AAATTTCTTGGGACAAAGGCTGTCCGACACGCTCTAGCAGTGCACAGTGCACAGTACGAG 900
Db 982 aaatttcttgggacaagggcctgtccgacacgcctacagctg9ccacgttacgagag 1041
QY 901 GAGAACGAATATGAAGTCCACGTGATGACCAAGCCATCAACAAGCCCATCAACTAC 960
Db 1042 gagaacgaatgatgaagtcacacgtgacacagccatcaacacacacacacacacacacac 1101
QY 961 CTGGGGCGGAGTCCCTGCGCCGCTGTGTCAGAGCGCCCGGGGGTTCGAGAGTGCTC 1020
Db 1102 ctg999g9cgagtcctctg9ccg9ctg9gcagacgc9cc9cc9cc9cc9cc9cc9cc9cc 1161
QY 1021 CCGGTATCAGCCCGATGATACAGTGCACACA ---GGCGCTCGGAGGCGCACCCGCGCTCC 1077
Db 1162 ccggttcacagcccgatgtaccagctgcacaagccgctgcg99gagc9cc9cc9cc9cc9cc 1221
QY 1078 AACCACTCGGCCAGGACAGCGCGTGTGAGTACCTGTGCTGTCTCTCAAGGCCAAGTTG 1137
Db 1222 aaccactcg9cc9gagcagc9cc9gagtcacgtgtgctgtgtgtgtgtgtgtgtgtgtgtgtgt 1281
QY 1138 GTGCCCTCGGAGCGGAGCGCTCCCGAGCAACAGCTGCCAAGACTCCACGAGCACCGAG 1197
Db 1282 gtg9cc9gagc9g9 1341
QY 1198 AGCAACACAGGAGGACCGCGAGCGGCTTATCTACTGTGACCAACACACATGCGCCGACGC 1257
Db 1342 agcaacaacag99gagc9g9 1397
QY 1258 CGCG ---AACCGCTGTGCTCAAGGAGGAGCACCGCGCTACGACCTGTGCGCGCGCC 1314
Db 1402 gcgcgcaacg9ctgtgcgtcaagagagagc9cc9cc9cc9cc9cc9cc9cc9cc9cc9cc9cc 1461
QY 1315 TCCGAGACTCCGAGGAGCGGCTCCCGTGTGTCAGCACACCGGGGAGCAGATGAAGGTG 1374
Db 1462 tc99g9aactc9g9 1521
QY 1375 TACAAGTGGCAAACTCCCGGGTGTCTTCTGTGATCAGTACACCTGTACACCATCCACATG 1434
Db 1522 tacaagtgc9aaacactgc99g9 1581
QY 1435 GGCTGCCACCGCTTCGCTGTATCTTTTGTAGTCAACATGTGCGGCTTACCACAGCCAGGAC 1494
Db 1582 g9ctg9ccag9cttc9ctg9atc9ctt9ct9ct9ct9ct9ct9ct9ct9ct9ct9ct9ct9ct9 1641
QY 1495 CGGTACGAGTTCGTGCGACATTAAGCGAGGGAGCAGCGCTTCCACATGAGCTAA 1551
Db 1642 c9gtacag9ttc9ct9gcacataac9g9g9g9g9g9g9g9g9g9g9g9g9g9g9g9g9g9g9g9 1698

RESULT 3

US-09-023-655-923
; Sequence 923, Application US/09023655
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart

QY	841	AAATTTCTTGGGGACAAGGCGCTGTCCGACACGCGCCTACGA---CAGTGCACGTACGAG	897
Db	1274	aaattctttggggacaagggcctgtccgacacgcctcagcagcgcgcagctacgag	1333
QY	898	AAGGAGAACGAATGATGAAGTCCACGTGTGGACCAAGCCATCAACAAGCCATCAAC	957
Db	1334	aaggagaacgaaatgatgaagtcccaactgtatggaccaagccaTcaacaacgccaatac	1393
QY	958	TACCTTGGGGCCGAGTCCCTGCGCCCGTGTGTGCAGACGCCCCCGGCGGTTCCTCGAGGTG	1017
Db	1394	tacctggggccgagtcctctggcgccgtggTgcagacgcgcgcgcgggttcctgaggtg	1453
QY	1018	GTCCCGGTTCATCAGCCCGATGTACCAGCTGCACA---GGCGCTCGGAGGGCACCCCGCGC	1074
Db	1454	gtcccggttcatacagcccagatgTaccagctgtcacaaagcgtctcgaggaggcaccccgcgc	1513
QY	1075	TCAACCACTTCGGCCCGACGACAGCCCGCTGGAGTACCTGTGTCTCTCAAGGCCAAG	1134
Db	1514	tcaaacactctggccaggacagcgcgtggagaacctgtgctgtctccaaggccaag	1573
QY	1135	TTGGTGCCCTTCGGAGCGGAGCGTCCCGGAGACAGCTGCCAAGACTTCACGGGACCC	1194
Db	1574	tTggTgcctctggagcgcgagggcgtcccccagacaaagcgtctaagaactccacggacac	1633
QY	1195	GAGACAACAACGAGGAGCAGCGACGGTCTTATCTACCTGTACCAACCATCTGCCCGCA	1254
Db	1634	gagagcaacaacgaggacgcagcggctctcatctaccagcaaccaatctgcgcccg	1693
QY	1255	CGCGCGC---ACGCGTGTGCTCAAGGAGGAGCACCGCGCTTACGACCTGTGCGCGCC	1311
Db	1694	cacgcgcgaacggtctgcctcaaggaggagcacgcgcctacacactgtctgcgcgc	1753
QY	1312	GCCTCGGAATCTCGAGGACGCGCTCCGCGTGTCTAGCACACGCGGGAGCAGATGAAG	1371
Db	1754	gcctccgaaactcgcaggacgcgcctccgcgtggTcagcaaccagcggggagcagatgaag	1813
QY	1372	GTGTACAAGTGGCAACTGCGCGGTGTCTTCTGTGATCAGCTCATGTACACCATCCAC	1431
Db	1814	gtgtacaagtgcgaactgcgcgggtgctctctcgtatcaegtcagtTlacaccaTccac	1873
QY	1432	ATGGGCTGCCGGCTCCGTGATCTTTTGTAGTGAACATGTTCGGCTTACCACACGCCAG	1491
Db	1874	aTgggctgccacgcttcctgTaatctttTgagtgaacaatgtgcggcttaccacagccaag	1933
QY	1492	GACCGGTACGAGTCTCTGCTCCACATTAACCGGAGGGGAGCACCGCTTCCACATGAGCTAA	1551
Db	1934	gaccggtacaggtctcgtgcataaacgcgaggaggacacgcgtctccacagactaa	1993

```

RESOLUT /
US-09-652-816-9158
; Sequence 9158, Application US/09652816
; GENERAL INFORMATION:
; APPLICANT: Gutierrez-Ramos, Jose-Carlos
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 1600.1177-001
; CURRENT APPLICATION NUMBER: US/09/652,816
; CURRENT FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/152,111
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 9647
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9158
; LENGTH: 4786
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(4786)
; OTHER INFORMATION: n = A,T,C or G
US-09-652-816-9158

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Query Match		94.7%;	Score 1468.8;	DB 25;	Length 4786;
Best Local Similarity		97.7%;	Pred. No. 1.8e-297;		
Matches 1524;		Conservative	0;	Mismatches	27; Indels 9; Gaps 3;
QY	1	ATGGATGTGACGAGGGTCAAGACATGCTCTTCATCAGGGAAGAAAGCCCTCTGTA	60		
Db	434	atggatgtgtagaggtcaagacatgtcccaagtttcagggaagaaagccccctgta	493		
QY	61	ACGGATCTCCAGATGAGGGGATGAGCCCATGCCGATGCCGAGAGACTCTCCACACACC	120		
Db	494	acgcatactcccsaga tgaaggcgatgagcccatgcccga tcccccgaggacctctccaccacc	553		
QY	121	TCGGGAGGACAGCAAGCTCCAAAGTGCACAGAGTGTGGCCAGTAATGTAAAGTAGAG	180		
Db	554	tcgggaggacagcaaaagctccaaagagtacagagtcgtggccagtaattgttaaagttagag	613		
QY	181	ACTCAGATGATGAAGAGAAATGGCGTGCCTGTGAATGAATGGGGAAGAATGTGCGGAG	240		
Db	614	actcagagtga tgaagagaatggcgctgctgtgaaa tgaatggggaagaaatgtgcggag	673		
QY	241	GATTACGAATCTTCATGCCCTCGGGAGAGAAATGAATGGCTCCCAAGGACCAAGGC	300		
Db	674	gatttacgaatctgatgcctcgggagagaaaatgaaatggctcccaacagggaccaaggc	733		
QY	301	AGCTGGCTTTGTCGGGAGTTGGAGGCATTGCACTTCCTTAAGGAAACTTAAAGTGTGAT	360		
Db	734	agctggcctttgcgggagttggaggatcctgactctcctaaagaaaactaaagtgtgat	793		
QY	361	ATCTGTGGGATCATTTGCAATCGGGGCCAATGTGCTCATGGTTTCAAAAGAACCCACT	420		
Db	794	atctgtggatcatttgcatcggcccaatgtgctcatggttcacaaagaagccacact	853		
QY	421	GGAGACGGCCCTTCAGTGCATGATGTCGGGGCTCATTCACCCAGAGGGCAACCTG	480		
Db	854	ggagaacggcccttcagtgcaatcagtcggtgcggtcctcattccaccdaagggcaacctg	913		
QY	481	CTCCGACATCAAGCTGATTCGGGGAGAACCCCTTCAAAATGCCACTCTGCAACTAC	540		
Db	914	ctccggacatcaagctgctattccctggggagaaagcccttcaaatgccaacctctgcaactac	973		
QY	541	GCCTGCCCGGGAGGACGCCCTCACTGTGCCACCTGTGAGAGCAGCTCCGTTGGTAAACT	600		
Db	974	gcctgcccgcggaggacgccctcactggccactgagacgcaactccgttggtaacct	1033		
QY	601	CACAATGTGGATATTGTGGCCGAACCTATAACAGCGAAGCTTTAGAGGAACATAAA	660		
Db	1034	cacaaatgtgga tatgtgcccgaagctataaacagcggaagctctcttagaggaaacataaa	1093		
QY	661	GAGCGTGCACAACTACTTGGAAAGCATGGGCTTTCCGGGACACTGTACCAGTCAAT	720		
Db	1094	gagcgtgcacaactactgtgaaagcatggccttcggggcacactgtaccagtcatt	1153		
QY	721	AAAGAGAAACTAAGCACAGTGAATGTGGCAGAGAGCTGTGCAAGTAGATCAGAGAG	780		
Db	1154	aaagaagaaactaatcacagtgaatggcagaagacctgtcaagatagatcacagaga	1213		
QY	781	TCTCTGCTGTGACAGACTAGCAAGTGAATGTGCGCAACAGTAAAGAGCTCTATGCTCTAG	840		
Db	1214	tcctctgtgtgacagagactagcaagttaacgttcgcacaaagcttaagctctatgcctcag	1273		
QY	841	AAATTTCTTGGGACAGGGCCCTGTCCGACACGCCCTACGA---CAGTCCCACTACGAG	897		
Db	1274	aaatttctgggacaagggcctgtccgacacgccctcctacgacagcgccagctacgag	1333		
QY	898	AAGGAACCAATATGATGAAGTCCCGATGGACCAACCATCAACAGCCATCAAC	957		
Db	1334	aaggagacgaaatgatgaagtccacgtgatggaccaagccatcaacaacgccaaccaac	1393		
QY	958	TACCTGGGGCCGAGTCCCTGCGCCGCTGGTGCAGACGCCGCCCGCGGCTTCCGAGGTG	1017		
Db	1394	tacctggggccgagtcctctgcgccgcgtgtgtcagacgccccccggcggttccgaggtg	1453		

QY	1018	GTCCCGGTTCATCAGCCCGGATGTACCAGCTGCACA---GGCGCTCGGAGGGCACCCCGCGC	1074		
Db	1454	gtcccggttcacagcccgatgtaccagctgcacaaagccctcgcggaggggcaaccccgcg	1513		
QY	1075	TCCAACACTTCGGCCCGACGAGCGCGCTGGAGTACTCTGCTGCTCTTCCAAAGGCCAAG	1134		
Db	1514	tcaaacactcggcccgagacagcgctggagaacctgtgctgtctccaaggccaag	1573		
QY	1135	TGCGTGCCTTCGAGCGGAGCGGCTCCCGAGCAACAGCTGCAAGACTCCACGGACACC	1194		
Db	1574	tgggtgccttcgagcgagggcgctcccgagcaacagctgtcaagactccacggacacc	1633		
QY	1195	GAGAGCAACCAACGAGGAGCGAGCGGTCTTATCTACTGTACCAACACATTCGCCCGA	1254		
Db	1634	gagagcaaacacagagagcgagcgctcctcatctacctgaccaacacacatcgcccg	1693		
QY	1255	CGCGCGC---AACCGCTGTGCTCAAGGAGGAGCACCGGCCCTACACCTGTGCGCGCC	1311		
Db	1694	cacgcgcgcaacgctgtctcgtcaaggaggagcacgcgcctacacactgtgcgcgc	1753		
QY	1312	GCCTCCGAGAACTCGCAGGAGCGCTCCGCGTGGTCAGCACACGCGGGAGCAGATGAAG	1371		
Db	1754	gcccccgagaaactcgcagagcgctcccgctggtcagcacacgcgggagcagatgaag	1813		
QY	1372	GTGTACAAAGTGCAGAACTGCCGGGTGCTTCTCTGGATCAGCTCATGTACACCATCCAC	1431		
Db	1814	gtgtacaagtgcgaacactgccgggtgctctctctggtacacgtcatgtacacatccac	1873		
QY	1432	ATGGGCTGCCACGGTTCCTGATCTTTTGTAGTGAACATGTGCGGCTACCAACAGCCAG	1491		
Db	1874	atggctgcgcacggctcccgatcctcttctgagtgcaacatgtgcggctaccacagccag	1933		
QY	1492	GACCGGTACGAGTCTCTCGTCACATAACCGGAGGAGCACCGCTTCCATGACGCTAA	1551		
Db	1934	gaccggtacagttctcgtcgcacataacgcgaggggagcaccgcttccacatgagctaa	1993		

RESULT 8

US-09-698-013-6274

Sequence 6274, Application us/09698013

GENERAL INFORMATION:

APPLICANT: Gearing, David P.

APPLICANT: Comrack, Christopher

APPLICANT: Kingsbury, Gillian A.

APPLICANT: Holtzman, Douglas A.

TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES

TITLE OF INVENTION: THEREFOR

FILE REFERENCE: 1600, 2013-001

CURRENT APPLICATION NUMBER: US/09/698,013

CURRENT FILING DATE: 2000-10-27

PRIOR APPLICATION NUMBER: 60/162,360

PRIOR FILING DATE: 1999-10-29

NUMBER OF SEQ ID NOS: 7935

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 6274

LENGTH: 4786

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc.feature

LOCATION: (1)...(4786)

OTHER INFORMATION: n = A,T,C or G

US-09-698-013-6274

Query Match

Best Local Similarity

Score 1468.8;

Pred. No. 1.8e-297;

Matches 1524;

Conservative

0;

Mismatches

27;

Indels

9;

Gaps

3;

QY

1

ATGGATGTGACGAGGGTCAAGACATGCTCTTCATCAGGGAAGAAAGCCCTCTGTA

60

Db

434

atggatgtgtagaggtcaagacatgtcccaagtttcagggaagaaagccccctgta

493

QY

61

ACGGATCTCCAGATGAGGGGATGAGCCCATGCCGATGCCGAGAGACTCTCCACACACC

120

Db

494

acgcatactcccsaga tgaaggcgatgagcccatgcccga tcccccgaggacctctccaccacc

553

QY

121

TCGGGAGGACAGCAAGCTCCAAAGTGCACAGAGTGTGGCCAGTAATGTAAAGTAGAG

180

Db

554

tcgggaggacagcaaaagctccaaagagtacagagtcgtggccagtaattgttaaagttagag

613

QY

181

ACTCAGATGATGAAGAGAAATGGCGTGCCTGTGAATGAATGGGGAAGAATGTGCGGAG

240

Db

614

actcagagtga tgaagagaatggcgctgctgtgaaa tgaatggggaagaaatgtgcggag

673

QY

241

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300

Db

674

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733

QY

301

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360

Db

734

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QY

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420

Db

794

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853

QY

421

GGAGACGGCCCTTCAGTGCATGATGTCGGGGCTCATTCACCCAGAGGGCAACCTG

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854

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913

QY

481

CTCCGACATCAAGCTGATTCGGGGAGAACCCCTTCAAAATGCCACTCTGCAACTAC

540

Db

914

ctccggacatcaagctgctattccctggggagaaagcccttcaaatgccaacctctgcaactac

973

QY

541

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600

Db

974

gcctgcccgcggaggacgccctcactggccactgagacgcaactccgttggtaacct

1033

QY

601

CACAATGTGGATATTGTGGCCGAACCTATAACAGCGAAGCTTTAGAGGAACATAAA

660

Db

1034

cacaaatgtgga tatgtgcccgaagctataaacagcggaagctctcttagaggaaacataaa

1093

QY

661

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720

Db

1094

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1153

QY

721

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780

Db

1154

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1213

QY

781

TCTCTGCTGTGACAGACTAGCAAGTGAATGTGCGCAACAGTAAAGAGCTCTATGCTCTAG

840

Db

1214

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1273

QY

841

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897

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1274

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1333

QY

898

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1393

QY

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1017

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1394

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1453

QY 61 AGCGATACCTCCAGATGAGGGCGATGAGCCCATGCCGATCCCGAGGACCTCTCCACCACC 120
Db 494 agcgatactccagatgagggcgatgagcccatgcgatcccgagagccctccaccacc 553
QY 121 TCGGGAGGACAGCAAGCTCCAGAGTGCACAGTCTGGCCAGTAAATGTTAAAGTAGAG 180
Db 554 tcggggagacagcaaaagctccaaagtgacagagtcgtggccagtaattgttaagtagag 613
QY 181 ACTCAGAGTATGAAGAGAAATGGCGTGTGAAATGAATGGGAAGAAATGTGGGAG 240
Db 614 actcagagtgatgaagaaatggggcgatgagtgaaatgaaatggggagaaatggtcgag 673
QY 241 GATTACGAAATGCTGATCGCTCGGGAGAGAAATGAATGGCTCCACAGGACCAAGGC 300
Db 674 gattacgaatgctgatcgctcgggagagaaatgaatggctccacagggaccaaggc 733
QY 301 AGCTCGGCTTGTGCGGAGTGGGACATTCGACTTCCTAACGGGAAACTAAAGTGTGAT 360
Db 734 agctcggcttgtcgggagttggaggaatcgacttcctaaacgggaaactaaagtgtgat 793
QY 361 ATCTGTGGGATCATTTGCACTCGGGCCCAATGTGCTCATGTTTCAAAAAGAGCCACACT 420
Db 794 atctgtggatcatttgcacggcccaatgtgctcatgtttcacaagaagaccacact 853
QY 421 GGAGAACGGCCCTTCAGTGCATCAGTCGGGGCCCTCATTCACCCAGAAAGGCAACCTG 480
Db 854 ggagaaacggcccttcagtgcaatcagtgcggggctcattcaccacgaagggcaacctg 913
QY 481 CTCCGGCACATCAAGCTGCATTCCGGGAGAGAGCCCTTCAATGCCACCTCTGCACACTAC 540
Db 914 ctccggcacatacagctgcatcccgggagagcccttcaaatgccaactctgcaactac 973
QY 541 GCTGCGCGGAGGAGGCCCTCACTGCGCCACCTGAGGACGCACTCGGTTGGTAAACCT 600
Db 974 gctgpcgcggagggagccctcactggccactgagagcactccgttggtaacct 1033
QY 601 CACAATGTGGATATGTGGCGAGCTATAACAGAGCAAGCTCTTTAGAGAAACATAAA 660
Db 1034 cacaatgtggatattgtggcgaagctataaacagcgaagctctttagagaaacataaa 1093
QY 661 GAGCGTGCCACAACTACTTGTGAAGCATGCGCCCTTCCGGGACACTGTACCCAGTCAAT 720
Db 1094 gagcgtgcacaactacttgaaagcatggccttcgggcacactgtaccagtcatt 1153
QY 721 AAAGAGAAACTAAGCACAGTGAATGGCAGAACCTGTGCAAGATAGGATCAGAGAGA 780
Db 1154 aaagagaaactaatcacagtgaaatggcagagacctgtgcaagataggtacagagaga 1213
QY 781 TCTCTCGTGTGACAGACTAGCAAGTAAATGCGCAACGTAAGAGCTCTATGCCCTCAG 840
Db 1214 tctctcgtgtgtgagacagactagcaagtaacgtcgcaaacgttaagagctctatgctcag 1273
QY 841 AAATTTCTTGGGACAAAGGGCTGTCCGACAGCGCCCTACGA---CAGTGCACCGTACGAG 897
Db 1274 aaatttcttgggacaaagggcgtgccacagccctacgacagcagcgccagtaacag 1333
QY 898 AGGAGAACGAAATGATGAATGCCACGTGATGACCAAGCAATCAACAGCCCATCAAC 957
Db 1334 aaggagaaacgaatgatgaatgccacgtgtgagaccagccatcaacaaacgcacatcaac 1393
QY 958 TACCTGGGGCGGCGAGTCCGCTGCGCCGCTGTGTGACAGCGCCCGGGGTTCCGAGGTG 1017
Db 1394 tacttggggggccgagtcctcgccgcgtgtgtgagacgccccggcggttccgaggtg 1453
QY 1018 GTCCGGGTATACGCCGATGTACAGTGTGACA---GGCGCTGGGAGGGCACCCCGCGC 1074
Db 1454 gtcccgggtcaatcagcccgatgtaccagctgcacaagcgctcgcgagggcaccgccgcg 1513
QY 1075 TCCAACTACTCGGCCCGGACAGCGCCCTGAGTACCTGTGCTCTCCAAAGGCCAAG 1134
Db 1514 tccaaactactcgcccgagacagcgccgtggagaaacctgctgctctccaaagggccaag 1573

QY 1135 TTGTGTCCCTCGGAGCGCGAGCGCTCCCGAGCAACAGCTGCCAAGACTCCACAGCACCC 1194
Db 1574 ttggtgcctcgagcgagcgagcggtcccgagcaaacagctgtcaagactccacgagacacc 1633
QY 1195 GAGAGCAACACAGAGGAGGACGCGAGCGGTCTTATCTACCTGACCAACACATCGCCGGA 1254
Db 1634 gagagcaacaacagggagcagcgagcggtctctctacctgacccaaccacatcgccccg 1693
QY 1255 CGCGGCG---AACGCTGTGCTCAAGGAGGAGCAGCGCGCTACGACCTGCTCGCGGCC 1311
Db 1694 cacgcygcgaacgctgtctgctcaagagagcaccgcgcttacgacctgtcgcgccc 1753
QY 1312 CCTCCGAGAACTCGCAGGACGCGCTCCGCTGCTGACGACACGCGGGAGGACAGTCAAG 1371
Db 1754 gctccgagaaactcgagcagcgctcggtggtcagcaccagcgggagcagatgaag 1813
QY 1372 GTGTACAAGTCGGAACACTGCCGGGTGCTCTTCTGATCAGTCATGTACCATCCAC 1431
Db 1814 gtgtacaagtgcgaacactgcgggtgctctctctggtatcagctcatgtacaccatcac 1873
QY 1432 ATGGCTGCCACGCTTCCGCTGATCTTTGAGTGCAACATGTGCGGCTACCCAGCCAG 1491
Db 1874 atgggctgcgaacgcttccgtgataccctttgagtcgaacatgtcggtctaccacagccag 1933
QY 1492 GACCGTACGAGTCTCTCCGACATAACGCGGGGAGGACCGCTTCCACATGAGCTAA 1551
Db 1934 gaccggtacgagttctcgtcgacataacgcgaggggagcaccgcttccacatgagctaa 1993
RESULT 9
US-09-698-014-4890
; Sequence 4890, Application us/09698014
; GENERAL INFORMATION:
; APPLICANT: Gearing, David P.
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Kingsbury, Gillian A.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: 1600.2014-001
; CURRENT APPLICATION NUMBER: US/09/698,014
; PRIORITY FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: 60/162,363
; PRIORITY FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 6098
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4890
; LENGTH: 4786
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(4786)
; OTHER INFORMATION: n = A,T,C or G
US-09-698-014-4890

Query Match 94.7%; Score 1468.8; DB 27; Length 4786;
Best Local Similarity 97.7%; Pred. No. 1.8e-297;
Matches 1524; Conservative 0; Mismatches 27; Indels 9; Gaps 3;

QY 1 ATGATGCTCAGCAGGGTCAAGACATGTCTTTCTCATCAGGGGAAGAAAGCCCTCTGTA 60
Db 434 atgagtctgatgaggtcaagacatgtcccaagatttcagggaagaaagccccctgta 493
QY 61 AGCGATCTCCAGATGAGGCGATGAGCCCATCCGATCCCGAGGACCTCTCCACACC 120
Db 494 agcgatactccagatgagggcgatgagcccatgccgatccccgaggaacctctccaccacc 553
QY 121 TCGGGAGGACAGCAAGCTCCAAAGATGACAGAGTCTGTCGCCAGTAAATGTTAAAGTAGAG 180
Db 554 tcggggagacagcaaacgctccaaagtgacagagtcgtggccagtaattgttaagtagag 613
QY 181 ACTCAGATGATGAAGAGAAATGGCGTGTGCTGTGAAATGAATGGGGAAGAAATGTGGGAG 240

Qy	361	ATCTGTGGGATCATTTTGCAATCGGGCCCAATGTGCTCATGTGTTACAAAAGAGCCACACT	420
Db	794	atctgtgggatcatttgcattcgccccaatgtctcatgtttcacaagaagccacact	853
Qy	421	GGAGAACGGCCCTTCAGTGTGCATAGTCGGGGGCGCTCATTTCACCAGAGGGCAACTTG	480
Db	854	ggagaacggcccttcagtgcaatcagtgcggggctcattcaccagaagggcaactg	913
Qy	481	CTCCGGCACATCAAGTCGATTTCCGGGGAGAGCGCTTCAAATGCACCTCTCGCAACTAC	540
Db	914	ctcggcacatcaagctgcatccggggagaagcccttcaaatgccacctctcgcaactac	973
Qy	541	GCCCTGGCGGGAGGACGCCCTCACTGGCCACCTGAGGACGCACTCGGTGGTGAACCT	600
Db	974	gctcgccggcgaggagccctcactgccaactggacgctgagcgcgactcogtttggtaaacct	1033
Qy	601	CACAAATGTGGATATTGTGCGCGAAAGCTATAAACAGCGCAACGTCTTTAGAGGAACATAAA	660
Db	1034	cacaaatgtgatatattgtgcccgaagctataaacgcggaagctcttttagaggaaacataaa	1093
Qy	661	GACCGTGGCCACACTACTTTGGAAGCATGGGCGCTTCGGGCACACACTGTACCCAGTCATT	720
Db	1094	gagcgtgcacaactactcttggaaagcatgggcttcgcggcacaactgtaccgaagtcat	1153
Qy	721	AAAGAGAAACTAAGCACACAGTCAAAATGSCAGAGAACCTGTGCAAGATAGGATCAGAGAGA	780
Db	1154	aaagaagaactaatcaacagtgaatggcagaagaacctgtgcaagaTAGatcagagaga	1213
Qy	781	TCCTCTGCTGGACAGACTAGCAAGTAAATGTGCCAAACGTAAGAGCTCTATGCCCTCAG	840
Db	1214	tctctgtctggacagactagcaagtaacgtcgccaaacgtaagagctctatgctctcag	1273
Qy	841	AAATTCTTGGGCAAGGGCTGTCCGACAGCGCCTACGA--CAGTGCCACGTACGAG	897
Db	1274	aaatttcttg999acaa999ccgttcgcagacgcacctacgacagcgccagctacag	1333
Qy	898	AAGGAGACGAATGATGAAGTCCACGCTGATGGACCAAGCAATCAACAGCGCATCAAC	957
Db	1334	aaggagaacgaatgatgaagtcccacgtgatggaccaagccatcaacaagccataaac	1393
Qy	958	TACCTGGGGCGAGTCCCTGGCCCGCTGTGTGACAGCGCCCGGGCGGTTCGAGAGTG	1017
Db	1394	tacctg9999ccgagctccctcgccctgtgtgcagacgccccggcggtctccgaggtg	1453
Qy	1018	GTCCCGGTATCAGCCCGCATACCAAGTGTGACATGTCACACA--GGCGCTCGGAGGCAACCCCGCGC	1074
Db	1454	gtcccggtcatcagcccgatgtaccagctgcacaagcgcgtcgcgagggcaccgcgcgc	1513
Qy	1075	TCCACCACTCGGCCAGGACAGCGCGGTGAGTACCTGTGTCTCTCCAAGGCCAAG	1134
Db	1514	tccaacctcgcccgaggaacgcgcgtggagaacctgtgtgtctctccaggccaag	1573
Qy	1135	TTGGTGCCCTCGGAGCGGAGCGCTCCCGAGCAACAGCTGCCAAGACTCCACGGACACC	1194
Db	1574	tgggtgacctcgagcgcgagcgtccccagcaaacagtgtcaagactccaaggaacc	1633
Qy	1195	GAGACGACACGAGGACGCGGAGCGGTCTATTCTACCTGACCACCAACACATCGCCCCGA	1254
Db	1634	gagagcaaacagaggagcagcgagcgtctcatctacctgaccaaccaatcgccccg	1693
Qy	1255	CGCGCGC---AACGGCTGTGCTCAAGGAGGACCGCGCCTTACGACCTGTCTGCGCGCC	1311
Db	1694	caagcgcgaacagcgtctgtcgtctcaaggaggaacgcgcctacgacctgtgcgccgc	1753
Qy	1312	GCCTCCGGAATCTGCAGGACGCGCTCCGGTGGTTCAGACCAACGCGGGAGCAGATGAAG	1371
Db	1754	gctccggaactcgcagacgcgctccgctggtcagcaacgcg999gagcagatgaaag	1813
Qy	1372	GNGTACAGTCCGAACACTGCCGGTGCTCTTCTGTGATCACTGATACACATCCAC	1431
Db	1814	ggtacaagtcgaacctcg999gtctctcctggaatcagtcatgtacacatccaac	1873

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RESULT      11
US-09-726-802-2123
; Sequence 2123, Application US/09726802
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.
; APPLICANT: Falb, Dean A.
; APPLICANT:
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 1600.2025-001
; CURRENT APPLICATION NUMBER: US/09/726,802
; CURRENT FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 60/168,012
; PRIOR FILING DATE: 1999-11-30
; NUMBER OF SEQ ID NOS: 2872
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2123
; LENGTH: 4786
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(4786)
; OTHER INFORMATION: n = A,T,C or G
US-09-726-802-2123

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Query Match 94.7%; Score 1468.8; DB 29; Length 4786;
Best Local Similarity 97.7%; Pred. No. 1.8e-297;
Matches 1524; Conservative 0; Mismatches 27; Indels 9;

1	QY	ATGATGCTCAGCAGGGTCAAGACATGTCTTTTCTCATCAGGGAAGAAAGCCCCCTGTA	60
434	Db	atgagtctgatgagggccaagacatgtccaaagtctcagggaagaaagccccctgta	493
61	QY	AGCGTACTCCAGATCAGGCGCATGAGCCCATCCGATCCCGAGACCTCTCCACCAAC	120
494	Db	agcgatactccagatgaggcgatgagcccatgcccagaggaaacctctccaccacc	553
121	QY	TCGGGAGGACAGCAAGCTCCAGAGTGCACAGAGTGGTGCCCAAGTAATGTTAAAGTAGAG	180
554	Db	tcgggagagcagcaagctccaagatgcacagagtcgtggccagtatgttaaagttagag	613
181	QY	ACTCAGAGTCATCAACAGAAATGGCGTGCTGTGAAATGAATGGGGAAGAAATCTGCGGAG	240
614	Db	actcagagtgaagaagaatgggcgtgcctgtgaaatgaa1999gaaagaatgtgcgagag	673
241	QY	GATTTACGAATGCTTGATGCTCGGAGAGAAAATGAATGGTCCACAGGACCAAGGC	300
674	Db	gatttcagaaatgcttgatgcctcggagagaaaaatgaatggctccacagggaccaagagc	733
301	QY	AGCTCGGCTTTGTCGGAGTTGAGGSCATTCGACTTCCTTAACGGAAAACTAAAGTGTGAT	360
734	Db	agctcgcttctg1cggagcttggagca1ctcgactctctaa1cggaaaaactaa1tgtgat	793
361	QY	ATCTGTGGATCATTTGCATCGGGGCCAATGTGCTCATGGTTTCACAAAAGAAGCCACACT	420
794	Db	atctgtgggatcat1tgatcgatcgggcccaatgtgctcatgtttcaaaaagaagccacact	853
421	QY	GGAGACGCGCCCTCCAGTGCCAATCAGTCCGGGGCCTCATTTACCCAGAGGGCAACCTG	480
854	Db	ggagaacgccccctccag1tgcattcag1tgcgggggctcattcaccocgaagggcaactgt	913
481	QY	CTCCGGCACATCAAGTGCATTTCCGGGGAGAGGCCTTCAATGCGCACTCTGCAACTAC	540


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QY 661 GAGCGCTGCCAACAACACTTGTGGAAGCATGGGCTTCCGGGCACACTGTACCCAGTCAATT 720
Db 1094 gagcgtgcacaaactacttggaaagcatgggcttcgggcacactgtaccagtcatt 1153
QY 721 AAAGAAGAAACAAAGACACAGTGAATAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
Db 1154 aaagaagaactaatcacagtgaatggcagagagagagagagagagagagagagagagag 1213
QY 781 TCTCTCGTCTGACAGACTAGCAAGTAATATGTCGCAACAGTAAAGAGCTTATGCTCAG 840
Db 1214 tctctcgtctgacagactagcaagtaacgtagcgaagagagagagagagagagagagagag 1273
QY 841 AAATTCTTGGGACAAAGGCTTCCGACAGCCCTACGA---CAGTGCACAGTACGAG 897
Db 1274 aaattcttggggaagaagggctgtccgacagccctacgagcagcagcagcagcagcag 1333
QY 898 AAGGAGAAAGAAATGATGAAGTCCACAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGG 957
Db 1334 aaggagaagaatgatgaagtcccaagtgatggagagagagagagagagagagagagagagag 1393
QY 958 TACTTGGGGCCGAGTCCCTGGCCCGCTGTGTGACAGCCCGCGGCGGTTCGAGAGTG 1017
Db 1394 tacctgggggagctgtccctggcccgctgtgtgagagcggcggtcccgaggtg 1453
QY 1018 GTCCCGGTATCAGCCGATGTACAGAGTGCACA---GGCGCTCGGAGGGACCCCGGC 1074
Db 1454 gtcccggtatcagccgaggtaccagctgcacaagcgtgcgaggggagcagcccgcc 1513
QY 1075 TCCAACTACTGGCCCGAGGACAGCGCCGTGGAGTACCTGTCTGTCTTCCAAAGGCGCAAG 1134
Db 1514 tccaaactactggcccgagagcagcggctgtgagaaactgtgtgtctcgaagcgaag 1573
QY 1135 TTGTGTCCTCGGAGCGGAGCGGTCCCGGAGCAACAGCTCCCAAGACTCCACGGACACC 1194
Db 1574 ttgtggtcctcggagcggagcgggtcccgagcaacagctgtcaagactccagggacac 1633
QY 1195 GAGAGCAACAAAGAGGAGGAGCGAGCGGTCTTATCTACCTGACCAACCACTACGCGCGA 1254
Db 1634 gagagcaacaagagagcagcagcgggtctctctctctctctctctctctctctctctct 1693
QY 1255 CGCGGCG---AACGGTGTGCTCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1311
Db 1694 cagcggcgcaacggctgtgtctcaagagagagcagcggcctctctctctctctctctctct 1753
QY 1312 GCCTCCGAGAACTCGCAGGAGCGCTCGCGGTGTCTGACAGCAGGAGGAGGAGGAGGAGG 1371
Db 1754 gcctccgagaaactcgagagcggcgtcccggtgtgtcagcagcagcagcagcagcagcag 1813
QY 1372 GTGTACAAAGTGCAGAACTGCGCGGTGCTCTTCTGTGATCAGCTCATGTACACCATCCAC 1431
Db 1814 gtgtacaagtgcgaactgcccgggtgtctctctctctctctctctctctctctctctctct 1873
QY 1432 ATGGGCTGCCAGGCTTCCGTGATCTTTGAGTGAACATGTGCGGCTTACCAGCCAG 1491
Db 1874 atgggctgcccagggcttccgtgtacctttgtgtgaacatgtgctgtctctctctctctct 1933
QY 1492 GACCGGTACGAGTCTCTGTGCGACATAACGAGGGGAGGAGGAGGAGGAGGAGGAGGAGG 1551
Db 1934 gaccggtacgagttctctgtcgcacataacgcgaggggagcagcgttccacatgagctaa 1993
```

RESULT 13

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US-60-324-185-24401
; Sequence 24401, Application US/60324185
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preeti
; APPLICANT: Diep, Dinh
; TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING
; TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE
; TITLE OF INVENTION: POLYMORPHISMS IDENTIFIED THEREBY
; FILE REFERENCE: GX-0019-1 P
```

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; CURRENT APPLICATION NUMBER: US/60/324,185
; CURRENT FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 35862
; SOFTWARE: PERL Program
; SEQ ID NO 24401
; LENGTH: 6203
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 345320.3
US-60-324-185-24401
```

```
Query Match 94.0%; Score 1457.8; DB 71; Length 6203;
Best Local Similarity 97.8%; Pred. No. 3.8e-295;
Matches 1524; Conservative 0; Mismatches 27; Indels 10; Gaps 4;
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```
QY 1 ATGGATCTGACGAGGCTCAAGACATGCTTTCTCATCAGGGAAGAAAGCCCCCTGTGA 60
Db 169 atggtatgtaggggtcaagacatgtccaaagtttcagggaagaaagccccctgtga 228
QY 61 AGCGATCTCCAGATGAGGCGGATGAGCCCATCCGATCCCGAGGAGGAGGAGGAGGAGGAG 120
Db 229 agcgatctccagatgagggcgatgagccatgccatcccgaggacccctctccacac 288
QY 121 TCGGGAGGACAGCAAGCTCCAAAGAGTGACAGAGTCTGTCGCGCAGTAATGTTAAAGTAGAG 180
Db 289 tcgggagagacagaaagctccaaagatgacagagtgctggtccagtaatgtctaaagtagag 348
QY 181 ACTCAGAGTGTGAAGAGATGGCGTGTGCTGTGTAATGAATGGGGAAGAAATGTGCGGAG 240
Db 349 actcagagtgatgaagagaatggcgctgctgtgaaatgaatggggaagaatgtgcggag 408
QY 241 GATTTAGGAATGCTGATGCTCGGAGAGAGAAATGAATGAATGGGGAAGAAATGTGCGGAG 300
Db 409 gattcagaaatgctgtatgctcctcgaggagaaatgaatggctccacagggaccacagc 468
QY 301 AGCTCGGCTTTGTGGGAGTTGGAGGATTCGACTTCCTTAACGGA-AAACTAAAGTGTCGA 359
Db 469 agctcgcttctgtcgagggtgagagcattcgacttcttaacgagagaaactaaagtgtga 528
QY 360 TATCTGTGGATCATTTGGATCGGGCCCAATGTGCTCATGTGTTTCACAAAGAGGAGGAG 419
Db 529 tatctgtggatcatattgtcatcgggcccaatgtgtctcatggttcacaaagaagccacac 588
QY 420 TGAGAAACGGCCCTTCCAGTGAATCAGTGGGCGGCTCATTCACCCAGGAGGAGGAGGAGG 479
Db 589 tggagaaacggcccttccagtcacatcagtcgctggcggtccttccacagaggggcaacct 648
QY 480 GCTCGGCGACATCAAGCTCATTCGCGGAGAGAGGCGCTTCAATGCGCCTCTGCAACTA 539
Db 649 gctcggcgacatcaagctcatctcgggggagagcccttcaaatgccacctgtcaacta 708
QY 540 CGGCTGCGCGCGGAGGAGGCGCTTCACTGGCCACCTGAGGAGGAGGAGGAGGAGGAGGAG 599
Db 709 cgcttgcgcgcggagggagcgcctcactggccacctgaggacgcactcctgtgttaaacc 768
QY 600 TCACAAATGTGATATTGTGGCGGAGAGCTATAAAGAGGAGGAGGAGGAGGAGGAGGAGGAG 659
Db 769 tcacaaatgtgattgttggcggaagctataaagcgaagcgtctttagagaggaacataa 828
QY 660 AGAGCGCTGCCAACAATCTTGGAAAGCATGGGCTTCCGGGCGACACTGTACCCAGTCAAT 719
Db 829 agagcgctgccacaactacttggaaagcatggccttcggcgagcactgtaccacagtcac 888
QY 720 TAAAGAAGAACTAAGCAGACAGTGAATGGCAGAGACCTGTGCAAGATAGGATCAGAGAG 779
Db 889 taagaagaagaactaatcacagtgaaatggcagaagacccgtgcaagatagatcagagag 948
QY 780 ATCTCTGCTGTGGAGAGTACGAGTAAGTAATGTGCGCAACAGCTAAGAGCTCTATGCGCTCA 839
Db 949 atctctgtctggaacactagcaagtaacgtgcgcaaacgtgaagagctctctatgctctca 1008
```



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Db 961 aag9ccaaagctgggcccctcgagcgagcgagcggtcccccagcaacagctgccaagactcc 1020
QY 1186 ACGGACACCGAGAGCAACACAGGAGAGCAGCGCGGTCTTATCTACCTGACCAACAC 1245
Db 1021 acggacacgagagcaacaacagagagcagcgagcggtcttatctaccctgaccaaccac 1080
QY 1246 ATCCCGCGAGCGCGCAACGCGTGTCTCAAGAGGAGAGCACCGCGCTTACGACCTGTG 1305
Db 1081 atcgccgcagcgcgcaacgcgtgtcgctcaaggagagcagcgcgcctacgacctgtg 1140
QY 1306 CGCGCGCGCTCCGAGAACCGCAGGACGCGCTCCGCGTGTGAGCAGCACCGCGGAGCAG 1365
Db 1141 cgcgcgcctccgagaaactcgaggaacgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 1200
QY 1366 ATGAAGGTGTACAAGTGCAGAACACTGCCCGGTGCTCTTCTCGATCATGTCATACACC 1425
Db 1201 atgaaggtgtacaagtgcgaacactgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 1260
QY 1426 ATCCACATGGGTGCGACCGCTTCGCTGATCCTTTGAGTGCAACATGTGGCGCTACCAC 1485
Db 1261 atccacatgggtgcacgcgttcctcgatccttttgatgcaacatgtggcgctaccac 1320
QY 1486 AGCGAGACCGGTACGAGTCTCGTCGACATAACGCGAGGAGGACCGCTTCCACATG 1545
Db 1321 agccagacccggtacgagctctcgtcgcacataaacgcgaggggagcaaccgcttcacatg 1380
QY 1546 AGCTAA 1551
Db 1381 agctaa 1386

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RESULT 15

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US-08-238-212A-3
; Sequence 3, Application US/08238212A
; GENERAL INFORMATION:
; APPLICANT: Georgopoulos, Katia A.
; TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE
; NUMBER OF SEQUENCES: 164
; CORRESPONDENCE ADDRESS:
; ADDRESS: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, Suite 510
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII (text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/238, 212A
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 121,438
; FILING DATE: 14-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 946,233
; FILING DATE: 14-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Paul L.
; REGISTRATION NUMBER: 35,695
; REFERENCE/DOCKET NUMBER: MPG-006CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1386 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double

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; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1386
; US-08-238-212A-3

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Query Match 89.4%; Score 1386; DB 6; Length 1386;
Best Local Similarity 100.0%; Pred. No. 3.5e-280; Indels 0; Gaps 0;

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Matches 1386; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 166 AATCTTAAAGTAGAGACTCAGAGTGATCAAGAGAAATGGGCTGCTGTGAATGAATGGG 225
Db 1 AATCTTAAAGTAGAGACTCAGAGTGATCAAGAGAAATGGGCTGCTGTGAATGAATGGG 60
QY 226 GAAGAATGTGGGAGGATTTACGAATGCTTGTATGCTCGGAGAGAGAAATGAATGGCTCC 285
Db 61 GAAGAATGTGGGAGGATTTACGAATGCTTGTATGCTCGGAGAGAGAAATGAATGGCTCC 120
QY 286 CACAGGACCAAGCAGCTCGGCTTTCTCGGGAGTTGAGGAGTTCGACTTCCTTAACGGA 345
Db 121 CACAGGACCAAGCAGCTCGGCTTTCTCGGGAGTTGAGGAGTTCGACTTCCTTAACGGA 180
QY 346 AAATAAGTGTGATATCTGTGGGATCATTTGCATCGGGGCCCAATGTCTCATGGTTTAC 405
Db 181 AAATAAGTGTGATATCTGTGGGATCATTTGCATCGGGGCCCAATGTCTCATGGTTTAC 240
QY 406 AAAAGAGCCACACTGGAGAACGGCCCTTCAGTGCATCAATCAGTGGGGGCTCATTCACC 465
Db 241 AAAAGAGCCACACTGGAGAACGGCCCTTCAGTGCATCAATCAGTGGGGGCTCATTCACC 300
QY 466 CAGAAAGGCAACCTGCTCCGGGCACATCAAGCTGCATTCCGGGAGAGCCCTTCAATGC 525
Db 301 CAGAAAGGCAACCTGCTCCGGGCACATCAAGCTGCATTCCGGGAGAGCCCTTCAATGC 360
QY 526 CACCTCTGCACTACGCTTCCGGCGGAGGAGCCCTCACTGGCCACCTGAGAGCGCAC 585
Db 361 CACCTCTGCACTACGCTTCCGGCGGAGGAGCCCTCACTGGCCACCTGAGAGCGCAC 420
QY 586 TCCGTTGTAAACCTCAAAATGTGGATATTTGGCGGAAGCTATAAACAGCAAGCTCT 645
Db 421 TCCGTTGTAAACCTCAAAATGTGGATATTTGGCGGAAGCTATAAACAGCAAGCTCT 480
QY 646 TTAGAGGAACATAAAGAGCGCTGCCACAACTACTTTGAAAGCATGGGCTTCCGGGCACA 705
Db 481 TTAGAGGAACATAAAGAGCGCTGCCACAACTACTTTGAAAGCATGGGCTTCCGGGCACA 540
QY 706 CTGTACCCAGTCATTAAGAAGAACTAAGCAGTGAATGGCAGAACCTGTGTCAAG 765
Db 541 CTGTACCCAGTCATTAAGAAGAACTAAGCAGTGAATGGCAGAACCTGTGTCAAG 600
QY 766 ATAGGATCAGAGAGATCTCTGCTGGACAGACTAGCAAGTAATGTGCGCAACCTAAG 825
Db 601 ATAGGATCAGAGAGATCTCTGCTGGACAGACTAGCAAGTAATGTGCGCAACCTAAG 660
QY 826 AGCTCTATGCTCAGAAATTTCTTGGGAGCAAGGGCTGTCCGACACGCGCTTACGACGT 885
Db 661 AGCTCTATGCTCAGAAATTTCTTGGGAGCAAGGGCTGTCCGACACGCGCTTACGACGT 720
QY 886 GCCACGTACGAGAGAGAGAAATGATGAAGTCCAGCTGATGACCAAGCCATCAAC 945
Db 721 GCCACGTACGAGAGAGAGAAATGATGAAGTCCAGCTGATGACCAAGCCATCAAC 780
QY 946 AAGCCCATCAACTACCTTGGGGCGGAGTCCCTGCGCGCGTGGTGCAGACGCCCGCGGC 1005
Db 781 AAGCCCATCAACTACCTTGGGGCGGAGTCCCTGCGCGCGTGGTGCAGACGCCCGCGGC 840
QY 1006 GGTTCGAGGTGTCCCGGTCTATPACGCCCGGTATACAGCTGCACAGGCGCTCGGAGGC 1065
Db 841 GGTTCGAGGTGTCCCGGTCTATPACGCCCGGTATACAGCTGCACAGGCGCTCGGAGGC 900
QY 1066 ACCCGCGGCTCCCAACCACTCGGGCCAGGACAGCGCGGTGGAGTACTGCTGCTCTCTCC 1125

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Db 901 ACCCGCGCTCCAACTCGCGCCAGGACAGCGCGTGGAGTACCTGCTGCTCTCC 960
QY 1126 AAGGCCAAGTTGGTCCCTCGAGCGCGAGGCGTCCCGAGCAACAGCTGCCAAGACTCC 1185
Db 961 AAGGCCAAGTTGGTCCCTCGAGCGCGAGGCGTCCCGAGCAACAGCTGCCAAGACTCC 1020
QY 1186 ACGGACACCGAGAGCAACAAACAGGAGGAGCGCGCTTATCTACCTGACCAACAC 1245
Db 1021 ACGGACACCGAGAGCAACAAACAGGAGGAGCGCGCTTATCTACCTGACCAACAC 1080
QY 1246 ATGCGCCGACGCGCGCAACGCGTGTGCTCAAGGAGGAGCAACCGCGCTACGACCTGCTG 1305
Db 1081 ATGCGCCGACGCGCGCAACGCGTGTGCTCAAGGAGGAGCAACCGCGCTACGACCTGCTG 1140
QY 1306 CGCGCGCGCTCCGAGAACTCGGAGGAGCGGCTCCGCGTGGTCAGCAACGCGGGGAGCAG 1365
Db 1141 CGCGCGCGCTCCGAGAACTCGGAGGAGCGGCTCCGCGTGGTCAGCAACGCGGGGAGCAG 1200
QY 1366 ATGAAGGTGTACAAGTGCAGCACTGCCGCGTGTCTTCTCTGGATCAGCTCATGTACACC 1425
Db 1201 ATGAAGGTGTACAAGTGCAGCACTGCCGCGTGTCTTCTCTGGATCAGCTCATGTACACC 1260
QY 1426 ATCCACATGGGTGCCACCGGCTTCGCTGATCCTTTTGTAGTGCAACATGTGGGCTTACCAC 1485
Db 1261 ATCCACATGGGTGCCACCGGCTTCGCTGATCCTTTTGTAGTGCAACATGTGGGCTTACCAC 1320
QY 1486 AGCCAGGACCGGTACGAGTCTCGTGACATACCGGAGGAGCGCGCTTCCACATG 1545
Db 1321 AGCCAGGACCGGTACGAGTCTCGTGACATACCGGAGGAGCGCGCTTCCACATG 1380
QY 1546 AGCTAA 1551
Db 1381 AGCTAA 1386

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Job time: 6786 sec